

Algorithms for Genome Rearrangement
Summer 2017

Exercises

Exercise 02, 28.04.2017

1. Given permutation $\pi = (2 1 3 5 4)$, (4 P)
 - (a) calculate the reversal distance $srd(\pi)$
 - (b) find a sorting scenario, i.e. a sequence of reversals ρ_1, \dots, ρ_d such that $\pi \circ \rho_1 \circ \dots \circ \rho_d = \mathbf{id}$ and $srd(\pi) = d$.
2. Any two components of a permutation are either *disjoint*, *nested*, or *chained*, the latter meaning that they appear consecutively and share extremities of the same symbol/gene. A component tree of a permutation is defined as follows: (4 P)

Definition Given a permutation π and its components, the component tree T_π is constructed as follows:

- (a) Each component is represented by a round node. It is colored black if unoriented and white, otherwise.
- (b) Each maximal chain is represented by a square node, containing its children.
- (c) A square node is the child of the smallest component that contains the chain.

In calculating $srd(\pi)$, the offset for additional reversals needed to orient unoriented components can be computed by determining a *cover* of the component tree T_π that has *minimum* cost.

Definition A cover C of a component tree T_π is a collection of paths joining all the unoriented components of π , such that each terminal node of a path belongs to a unique path. A path is short if it contains only one component, otherwise it is long.

The cost $t(C)$ of a cover C is the sum of costs of all paths, whereby a short path has cost 1 and a long path has cost 2.

Consider permutation

$$\pi = (1 3 -8 7 -6 4 5 9 11 -13 10 -12 14 -2 15 17 22 18 20 19 21 23 28 24 26 25 27 29 16),$$

- (a) use the Java program `InversionVisualization` provided on the course website to draw $BG(\pi)$. You can download the file containing π here. Using $BG(\pi)$, construct the component tree T_π ;
- (b) find an optimal tree cover (i.e. a cover with minimum cost) for T_π .

Hand in solutions before tutorial on 05.05.2017